

Atty Dkt. No.: 10011076-1  
USSN: 10/087,035

### AMENDMENTS

Please incorporate the following amendments to the subject application.

In the Specification:

Please replace paragraph [0049] of the subject application with the following:

Databases 22a-22n may additionally comprise databases of genomic information that are accessible to the general public via the Internet. Such databases may include molecular, genetic, organism-based, gene expression, bibliographic, or other type of genomic information usable for selection of array design parameters. Public, Internet-accessible data bases that provide information usable in selection of array design parameters include the following, each of which can be accessed by entering "http:" (or "https:") plus "://" and the URL address (listed after each example) in the "address" window of an internet browser application (e.g., Netscape); by way of example, European Molecular Biology Laboratory Nucleotide Sequence Data Library (EMBL), <http://www.embl-heidelberg.de/>, DNA Database of Japan (DDBJ), <http://www.ddbj.nig.ac.jp/>, Genbank, <http://www.ncbi.nlm.nih.gov/Genbank/GenbankSearch.html>, Swiss-Prot., <http://www.expasy.ch/sprot/sprot-top.html>, Genome Database (GDB), <http://gdbwww.gdb.org>, Online Mendelian Inheritance in Man (OMIM), <http://www3.ncbi.nlm.nih.gov/Omim/>, Cellular Response Database, <http://LH15.umbc.edu/crd>, dbEST, <http://www.ncbi.nlm.nih.gov/dbEST/index.html>, GeneCards, <http://bioinformatics.weizmann.ac.il/cards/>, Globin Gene Server, <http://globin.cse.psu.edu>, Human Developmental Anatomy, <http://www.ana.ed.ac.uk/anatomy/database/humatl>, Kidney Development Database, <http://www.ana.ed.ac.uk/anatomy/database/kidbase/kidhome.html>, Merck Gene Index, [http://www.merck.com/mrl/merck\\_gene\\_index.2.html](http://www.merck.com/mrl/merck_gene_index.2.html), and Tooth Gene Expression Database, <http://bite-it.helsinki.fi/>. Proprietary databases are also accessible via the Internet for a fee or on a subscription basis, such as Incyte's LIFESEQ®, <http://www.incyte.com/sequence/index.shtml>, and DOUBLETWIST™, <https://genomezone.doubletwist.com/>. Various other public-accessible databases

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are known to those skilled in the art and may be used for databases 22a, 22b, 22n as well.

Please replace paragraph [0070] of the subject application with the following:

At event 140, the array vendor completes the array design process by providing any additional design parameters needed for completion of the array design that were not provided by the customer in events 110 and 120. Array design parameters that are selected or provided by the vendor will typically be associated with computationally complex aspects of array design, i.e., nucleic acid probe sequencing parameters. Event 140 accordingly includes sub-event 150 wherein sequence information for probe selection is obtained. Sequencing information may involve database searching using accession numbers for specific sequences, or use of database search algorithms such as FASTA or BLAST to obtain raw sequence data for the customer-selected genes of interest from event 100. The FASTA and BLAST algorithms, which are well known in the art, are approximate heuristic algorithms used to compute suboptimal pairwise similarity comparisons. Dynamic programming is used to compute a series of subsequence alignments that are combined to approximate a larger sequence alignment and global similarity score. (See, e.g., <http://www.ncbi.nlm.nih.gov/BLAST/>, both of which can be accessed by typing the listed URL into the "address" window of an Internet browser after "http:" plus "/").